

## Selection strategy for developing maize inbred lines with drought and disease resistance in Uganda

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### Abstract

Breeding for host plant resistance along with performance traits requires the use of an effective breeding method and selection strategy. Such a selection strategy and related indices should contribute to reducing the time required for breeding, and saving resources for further development and testing. This study of a maize (*Zea mays*) population identified efficient selection indices and a selection strategy for maize lines that combines selecting for traits of primary interest such as anthesis-silking interval (as a proxy for drought tolerance), and resistance to both *Turcicum* leaf blight (TLB) and maize streak virus (MSV) with other characteristics that directly and indirectly influence grain yield. Testcrosses were generated during the short rainy season of 2011 (August – December) at Kasese, with single cross (SC) testers from heterotic groups A and B used as males, planted in multiple rows, and pollen-bulked. F<sub>3</sub> lines were used as females, and planted ear-to-row in single-row plots. These crosses were then tested in three locations (Serere, Namulonge and Bulindi), in order to evaluate the performance of families in their early-segregating generations. Data was collected on a plot basis for: MSV, TLB (using rating scale 1 to 5), and ASI. The anthesis-silking-interval (ASI) was calculated from the difference between the silking and anthesis dates (ASI = SD – AD). Analysis of variance for single environments was based on lattice design using the linear mixed model procedure GENSTAT 14<sup>th</sup> edition.

**Key words:** Breeding for disease resistance, drought tolerance maize

### Résumé

La reproduction pour la résistance de la plante hôte avec traits de performance nécessite l'utilisation d'une méthode de sélection efficace et une stratégie de sélection. Une telle stratégie de sélection et indices connexes devraient contribuer à réduire le temps nécessaire à la reproduction, et d'économiser des ressources pour le développement et les tests. Cette étude d'un maïs (*Zea mays*), population identifiée d'indices efficaces de sélection et une stratégie de sélection des lignées de maïs qui combinent la sélection pour des caractères d'intérêt primaire tels que l'intervalle de la floraison des soies (comme un proxy pour la tolérance à la sécheresse), et la résistance à la fois à la bactérien de feuille *turcicum* (TLB) et le virus raie de maïs (MSV) avec d'autres caractéristiques qui influencent directement et indirectement le rendement en grain. Les tests de croisement ont été générés pendant la

courte saison des pluies de 2011 (août - décembre) à Kasese, avec des testeurs à croisement unique (SC) à partir de groupes hétéroclites A et B utilisés comme males, plantés en rangées multiples, et le pollen en vrac. Les lignés  $F_3$  ont été utilisés comme les femelles, et plantées épis par rangé dans les parcelles à simple rangé. Ces croisements ont ensuite été testés dans trois endroits (Sérère, Namulonge et Bulindi), afin d'évaluer la performance des familles dans leurs générations de ségrégation précoce. Les données ont été recueillies sur une base de l'intrigue pour MSV, TLB (en utilisant l'échelle d'évaluation de 1 à 5), et l'ASI. L'intervalle de la floraison des soies (ASI) a été calculé à partir de la différence entre la sortie des soies et les dates de floraison ( $ASI = SD - AD$ ). L'analyse de la variance pour les environnements simples reposait sur la conception du réseau en utilisant la procédure de modèle linéaire mixte GENSTAT 14<sup>ème</sup> édition.

Mots clés: sélection pour la résistance aux maladies, la tolérance à la sécheresse du maïs

## Introduction

Results for anthesis-silking-interval (ASI) showed a high frequency of  $F_2$  plants falling within the range of -3 to 0 days (67.4%), while only 29.2% of  $F_3$  families fell in the same range. In the inbreds, partial dominance conditioned for low disease pressure of TLB was indicated by 90% of  $F_2$  progeny and 81% of  $F_3$  progeny scoring resistant. In the  $F_3$  families, 63.4% showed resistance to MSV, suggesting both had some effect of segregation and a high response of the genotypes to environment. And selection among  $F_2$  and  $F_3$  progeny of a biparental cross has contributed to improvement of the performance of lines.

Significant GxE terms occurred frequently, but the GxE variance components were usually lower in magnitude than the pooled error (result presented in Table 1). Variance components for lines for yield (YLD), *Turcicum* leaf blight (TLB), maize streak virus (MSV), and anthesis silking interval (ASI) were larger than LxE interactions. Suggesting that early generation test-crossing could be a good strategy for developing hybrid maize with the desirable traits for yield, *Turcicum* leaf blight, maize streak virus, and drought tolerance (Table 1). Results showed high broad sense heritability (BSH) values across location. The relatively high

**Table 1. Multi-location analysis of variance.**

| Source of variation | df  | Yield              | TLB reaction       | MSV reaction       | ASI                |
|---------------------|-----|--------------------|--------------------|--------------------|--------------------|
| Line                | 57  | 1.39 <sup>ns</sup> | 0.29 <sup>sd</sup> | 109 <sup>sd</sup>  | 1.18 <sup>sd</sup> |
| Line * Environment  | 114 | 1.27 <sup>sd</sup> | 0.12 <sup>sd</sup> | 47.3 <sup>sd</sup> | 0.53 <sup>sd</sup> |
| Line*Tester         | 57  | 1.14 <sup>ns</sup> | 0.14 <sup>sd</sup> | 33.4 <sup>sd</sup> | 0.54 <sup>sd</sup> |
| Line*Env*Tester     | 114 | 1.20 <sup>sd</sup> | 0.08 <sup>sd</sup> | 20.1 <sup>ns</sup> | 0.36 <sup>sd</sup> |
| Pooled error        | 315 | 0.54               | 0.04               | 18.9               | 0.20               |
| Heritability        |     | 0.08               | 0.60               | 0.57               | 0.38               |

sd= significance different; ns= non-significant; ectively. ASI=Anthesis silking interval mean square; MSV=Maize streak virus incidence mean square; TLB=Turcicum leaf blight; YLD=Yield; Env\*Line=Environment, line interaction; Line x Tester x Env=Line, Tester, Environment interaction; df=degree of freedom

heritability makes the across environment selection for earliness easier on the basis of phenotype. Meanwhile, levels of heritability across locations were moderate for ASI, indicating the influence of environment on silking date.

Nine lines have been identified as the best, based on a consistent ranking correlated with maximum vigour in the hybrids in all four of the indices proposed, using ASI, yield and resistance to TLB and MSV as key components in the selection indices. These nine lines are WL-429-33; WL-429-40, WL-429-49; WL-429-37; WL-429-57; WL-429-34; WL-429-4, WL-429-50 and WL-429-119. The strategy used for the present study was to utilize all the indices developed, applying them from inbred development up through the testcrosses, tracking the best and most consistent genotypes.

### **Recommendation**

Recommendations emerging from this study include the use of effective blocking, , also since the across-environment mean for total yield indicated low heritability, which was probably due to little genetic variance among the parents used to derive the population, we recommends using diverse crosses to develop breeding populations, and then selecting for yield-per-plant in later generations.

In the present study we noted that selecting by the selection index in either the  $F_3$  generation or with the  $F_3$ -testcrosses was the best strategy for identifying the desirable individuals, and may improve the breeder's consistency in selecting the most promising lines with the best potential for multi-trait combination hybrid (as for MSV and TLB resistance, drought tolerance and high yield). And also noted that the highest gains for selection (>5%) are obtained when the selection is done at the testcross level, especially for traits with a high level of heritability in early stages (such as for MSV, TLB or ASI).

In the determination of heterotic group, results led us to conclude that there is no clear evidence supporting these lines belonging to heterotic group B, since most of them had SCA estimates of >1 SE in only one environment (14 lines in Serere) and 1 SE is not a very strong criterion to distinguish them, since 16% of lines (about 10 lines) are expected to have SCA values exceeding 1 SE by chance. However, there was a strong Line x Tester x Environment interaction, indicating the sensitivity to environmental influences of the performance of a specific line with a specific tester.

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### **References**

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